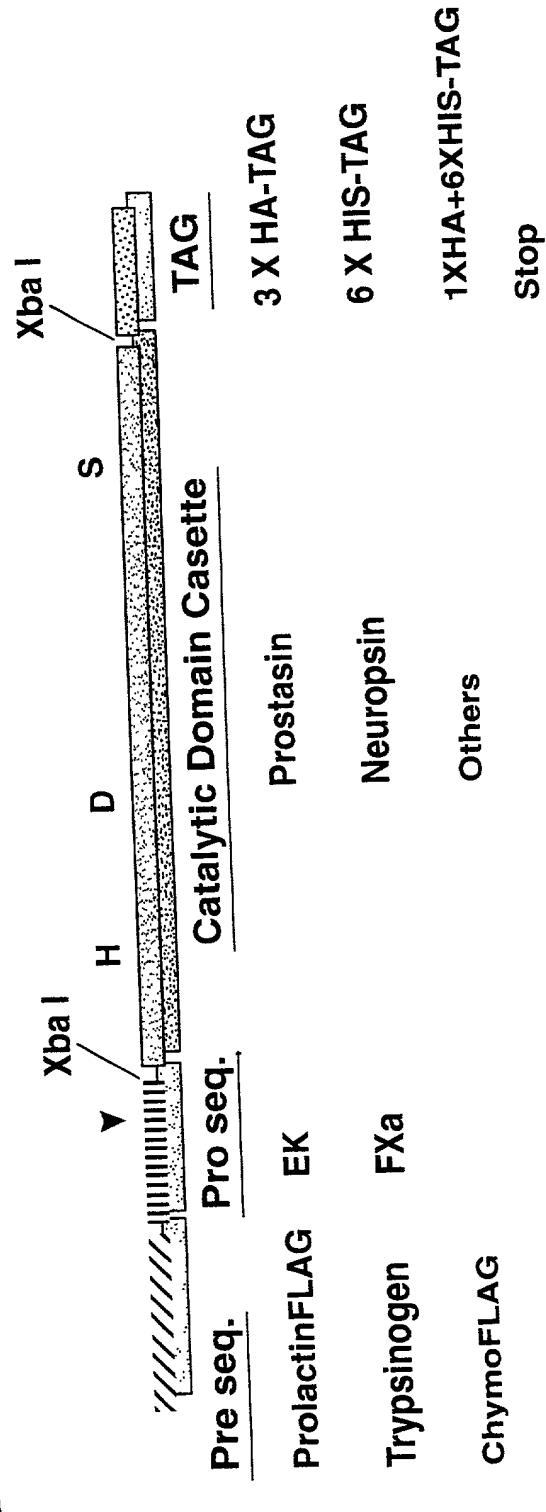


FIG. 1

SEQ.ID.NO.:1

FIG. 2(A)

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTCGTCGCAGAAATCCGCCTGCT
 -----+-----+-----+-----+-----+
 CTTAAGTGGTGGTACCTGCGTTCCAAGCAGCGCTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGTGTGGTCTCCG
 -----+-----+-----+-----+
 GGACGACGACCACCAAGTTAGATGAGAACACGGTCCCACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

100

101 ACTACAAGGACGACGACGTGGACGCGCCGCTTGCTGCCCTTT
 -----+-----+-----+-----+
 TGATGTTCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D V D A A A L A A P F
 FLAG EK2 Pro

150

151 GATGATGATGACAAGATCGTTGGGGCTATGCTCTAGATAGCGGGCCGCTT
 -----+-----+-----+-----+
 CTACTACTACTGTTCTAGCAACCCCCGATACGAGATCTATGCCGGCGAA
 D D D D K I V G G Y A L *
 EK2 Pro

200

201 CCCTTAGTGAGGGTTAATGCTCGAGCAGACATGATAAGATAACATTGAT
 -----+-----+-----+-----+
 GGGAAATCACTCCAATTACGAAGCTGCTGTACTATTCTATGTAAC
 SV40 Late pA

250

251 GAGTTGGACAAACCAACTAGAATGCAGTGAAAAAAATGCTTATTG
 -----+-----+-----+-----+
 CTCAAACCTGTTGGTGTGATCTACGTCACTTTTACGAAATAAAC
 SV40 Late pA

300

301 TGAAATTGTGATGCTATTGCTTATTGTAACCATTATAAGCTGCAATA
 -----+-----+-----+-----+
 ACTTTAACACTACGATAACGAAATAAACATTGGTAATATTGACGTTAT
 SV40 Late pA

350

351 HincII
 AACAAAGTTGAC
 -----+--- 361
 TTGTTCAACTG

FIG. 2(B)

SEQ. ID. NO.: 2

FIG. 2(C)

SEQ.ID.NO.:3

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAATCCCCTGCT
 CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGCTTT**AGGGCGGACGA**
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGT**GTGGTCTCCG**
 GGACGACGACCACCAACAGTTAGATGAGAACACGGTCCC**A**ACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

100

101 Not I

ACTACAAGGACGACGACGTGGACGCCGCTTGCTGCCCTTT
 TGATGTTCTGCTGCTGCTGCACCTGCCGGCGAGAACG**ACGGGGAAA**
 D Y K D D D D V D A A A L A A P F
 FLAG FXa Pro

150

151 Xba I

ATCGAGGGGCGCATTGTGGAGGGCTCGGATCTAGATA**ACCCCTACGATGTG**
 TAGCTCCCCGCGTAACACCTCCCAGCCTAGATCTATGGGGATGCTACAC
 I E G R I V E G S D L Y P Y D V
 FXa Pro

200

201

CCCGATTACGCCGCTAGATA**ACCCCTACGATGTGCCGATTACGCCGCTAG**
 GGGCTAATGCCGATCTATGGGGATGCTACACGGCTA**ATGCCGATC**
 P D Y A A R Y P Y D V P D Y A A R
 3 X HA-TAG

250

251

ATACCACTACGATGTGCCGATTACGCCGCTAGATA**ACCCCTACGATGTG**
 TATGGTGATGCTACACGGCTAATGCCGATCTATGGGG**ATGCTACACG**
 Y H Y D V P D Y A A R Y P Y D V
 3 X HA-TAG

300

301 Not I

CCGATTACGCCTAGCGGCCGCTTCCCTT**AGTGAGGGTTAATGCTCGAG**
 GGCTAATGCCGATGCCGGCGAAGGGAAAT**CACTCCAATTACGAAGCTC**
 P D Y A *

350

FIG. 2(D)

351 CAGACATGATAAGATAACATTGATGAGTTGGACAAACCACA**A**CTAGAATG
 -----+-----+-----+-----+-----+
 GTCTGTACTATTCTATGTAAC TACTCAAACCTGTTGGTGT**T**GATCTTAC
SV40 Late pA
 400

401 CAGTGAAAAAAATGCTTATTGTGAAATTGTGATGCTATTGCTTTATT
 -----+-----+-----+-----+-----+
 GTCACTTTTTACGAAATAAACACTTTAACACTACGATA**A**CGAAATAA
SV40 Late pA
HincII
 451 TGTAACCATTATAAGCTGCAATAAACAAAGTTGAC
 -----+-----+-----+
 ACATTGGTAATATTCGACGTTATTGTTCAACTG
484

6/34

FIG. 2(E)

SEQ.ID.NO.:4

Eco RI
GAATTCAACCACCATGGACAGCAAAGGTCGTCGCAGAAATCCGCCTGCT
1 CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTAGGGCGGACGA
M D S K G S S Q K S R L L
Prolactin Signal Sequence 50

CCTGCTGCTGGTGGTCAAATCTACTCTTGTGCCAGGGTGTGGTCTCCG
51 GGACGACGACCACCAAGTTAGATGAGAACACGGTCCCACACCAAGAGGC
L L L V V S N L L L C Q G V V S
Prolactin Signal Sequence 100

Not I
ACTACAAGGACGACGACGTGGACGCGGCCGCTTGCTGCCCTTT
101 TGATGTTCCCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
D Y K D D D D V D A A A L A A P F
FLAG EK1 Pro 150

Xba I
GATGATGATGACAAGATCGTTGGGGCTACAACTGTCTAGACATCACCAT
151 CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCTGTAGGGTA
D D D D K I V G G Y N C L H H H
EK1 Pro 200

Not I
CACCATCACTAGCGGCCGCTCCCTTAGTGAGGGTAATGCTTCGAGCA
201 GTGGTAGTGATGCCGGCGAAGGGAAATCACTCCAAATTACGAAGCTCGT
H H H *
6 X HIS-TAG 250

GACATGATAAGATACTTGATGAGTTGGACAAACACAACTAGAATGCA
251 CTGTACTATTCTATGTAACACTCAAACCTGTTGGTGTGATCTACGT
SV40 Late pA 300

GTGAAAAAAATGCTTATTTGTGAAATTGTGATGCTATTGCTTATTTG
301 CACTTTTTACGAAATAAACACTTAAACACTACGATAACGAATAAAC
SV40 Late pA 350

FIG. 2(F)

351	<u>HincII</u> TAACCATTATAAGCTGCAATAAACAAAGTTGAC -----+-----+-----+-----+ ATTGGTAATATTGACGTTATTTGTCAACTG	382
-----	--	-----

FIG. 2(G)

SEQ. ID. NO.: 5

Eco RI

1 GAATTCAACCACCATGGCTTCCTCTGGCTCCTCTCCTGCTGGGCCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGGAGAGGACGACCCGGGAGGA
 M A F L W L L S C W A L L
 Chymotrypsinogen Pre

50

51 GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACGACGACGACG
 CCCATGGTGGAAAGCCGACGCCAGGGGCTGATGTTCTGCTGCTGCTGC
 G T T F G C G V P D Y K D D D D |
 Chymotrypsinogen Pre FLAG

100

101 Not I CGGGCGCTCTGCTGCCCTTGATGATGATGACAAGATCGTTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTCTAGCAACCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

150

151 Xba I Not I TATGCTCTAGACATCACCATCACCATCACTAGCGGGCGCTTCCTTAGT
 ATACGAGATCTGTAGTGGTAGTGGTAGTGTGATCGCCGGCGAAGGGAAATCA
 Y A L H H H H H H *
 6 X HIS-TAG

200

201 GAGGGTTAATGCTCGAGCAGACATGATAAGATACTTGA~~T~~GAGTTGG
 CTCCCAATTACGAAGCTCGTCTGTACTATTCTATGTA~~ACT~~CAACCT
 SV40 Late pA

250

251 CAAACCACAACTAGAATGCAGTGAAAAAAATGCTTATTTGTGAAATTG
 GTTGGTGTGATCTACGTCACTTTTTACGAATAAACACTTTAAC
 SV40 Late pA

300

301 TGATGCTATTGCTTATTTGTAAACCATTATAAGCTGCAATAAACAAGTTG
 ACTACGATAACGAAATAAACATTGGTAATATTCGACGTTA~~T~~TTGTTAAC
 SV40 Late pA

350

351 II
 AC
 -- 352
 TG

FIG. 2(H)

SEQ.ID.NO.:6

Eco RI

1 GAATTCAACCACCATGGCTTCCTCTGGCTCCTCTCCTGCTGGGCCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGGAGAGGACGACCCGGGAGGA
 M A F L W L L S C W A L L
 Chymotrypsinogen Pre

50

51 GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACGACGACGACG
 CCCATGGTGGAAAGCCGACGCCAGGGGCTGATGTTCTGCTGCTGCTGC
 G T T F G C G V P D Y K D D D D |
 Chymotrypsinogen Pre FLAG

100

101 Not I

CGGCCGCTTGTGCTGCCCTTGATGATGATGACAAGATCGTTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTTCTAGCAACCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

150

151 Xba I

TATGCTCTAGATAACCCCTACGATGTGCCGATTACGCCGCTAGACATCAC
 ATACGAGATCTATGGGATGCTACACGGGCTAATGCCGATCTGTAGTG
 Y A L Y P Y D V P D Y A A R H H
 HA 6 X HIS-TAG

200

201 Not I

CATCACCATCACTAGCGCCGCTCCCTTAGTGAGGGTTAAATGCTTCGA
 GTAGTGGTAGTGATGCCGGCGAAGGGAAATCACTCCAATTACGAAGCT
 H H H H *

250

251 GCAGACATGATAAGATAATTGATGAGTTGGACAAACACAACTAGAAT
 CGTCTGTACTATTCTATGTAACACTCAAACCTGTTGGTGTGATCTTA
 SV40 Late pA

300

301 GCAGTAAAAAAATGCTTATTGTGAAATTGTGATGCTATTGCTTAT
 CGTCACTTTTTACGAAATAAACACTTAAACACTACGATAACGAAATA
 SV40 Late pA

350

10/34

FIG. 2(I)

HincII

351	TTGTAACCATTATAAGCTGCAATAAACAAAGTTGAC	385
	-----+-----+-----+-----+-----	
	AACATTGGTAATATTGACGTTATTTGTTCAACTG	

FIG. 3(A)

SEQ.ID.NO.: 7

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTCGTCGCAGAAAT CCCGCTGCT 50
 CTTAAGTGGTGGTACCTGCTCGTTCCAAGCAGCGTCTT **A**GGGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGCCAGGGT **G**TGGTCTCCG 100
 GGACGACGACCACCAACAGTTAGATGAGAACACGGTCCC **A**ACCCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

101 ACTACAAGGACGACGACGTGGACGCGCCGCTTGCTGCCCTTT 150
 TGATGTTCCCTGCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
 D Y K D D D D V D A A A L A A P F
 FLAG EK2 Pro

151 GATGATGATGACAAGATCGTTGGGGCTATGCTCTAGAGG CCGTCAGTG 200
 CTACTACTACTGTTCTAGCAACCCCCGATA CGAGATCTC CGGCCAGTCAC
 D D D D K I V G G Y A L E A G Q W
 EK2 Pro

201 GCCCTGGCAGGTCA GCATCACCTATGAAGGCGTCCATGT **G**T GTGGTGGCT 250
 CGGGACCGTCCAGTCGTAGTGGATACTTCCGCAGGTACAC **A**ACCCACGA
 P W Q V S I T Y E G V H V C G G
 Prostasin.CDS

251 CTCTCGTGTCTGAGCAGTGGGTGCTGTCAGCTGCTCACT **G**C TTCCCCAGC 300
 GAGAGCACAGACTCGTCACCCACGACAGTCGACGAGTGAC **G**AAGGGTTCG
 S L V S E Q W V L S A A H C F P S
 Prostasin.CDS

301 GAGCACCACAAGGAAGCCTATGAGGTCAAGCTGGGGCC **A**CCAGCTAGA 350
 CTCGTGGTGTTCCTCGGATACTCCAGTTGACCCCCGGG **T**GGTCGATCT
 E H H K E A Y E V K L G A H Q L D
 Prostasin.CDS

FIG. 3(B)

351 CTCCTACTCCGAGGACGCCAAGGTCAAGCACCCTGAAGGACATCATCCCC
 -----+-----+-----+-----+-----+
 GAGGATGAGGCTCCTGCGGTCCAGTCGTGGGACTTCTGTAGTAGGGGG
 S Y S E D A K V S T L K D I I P H
 Prostasin.CDS

401 ACCCCAGCTACCTCCAGGAGGGCTCCCAGGGCGACATTGCACTCCTCAA
 -----+-----+-----+-----+-----+
 TGGGGTCGATGGAGGTCCCTCCGAGGGTCCCGCTGTAACGTGAGGGAGTT
 P S Y L Q E G S Q G D I A L L Q
 Prostasin.CDS

451 CTCAGCAGACCCATCACCTTCTCCGCTACATCCGGCCATCTGCCTCCC
 -----+-----+-----+-----+-----+
 GAGTCGTCTGGGTAGTGGAGAGGGCGATGTAGGCCGGTAGACGGAGGG
 L S R P I T F S R Y I R P I C L P
 Prostasin.CDS

501 TGCAGCCAACGCCCTCTTCCCCAACGGCCTCCACTGCACTGTCACTGGCT
 -----+-----+-----+-----+-----+
 ACGTGGTTGCGGAGGAAGGGGTTGCCGGAGGTGACGTGACAGTGACCGA
 A A N A S F P N G L H C T V T G
 Prostasin.CDS

551 GGGGTCACTGGCCCCCTCAGTGAGCCTCTGACGCCAAGCCACTGCAG
 -----+-----+-----+-----+-----+
 CCCCAGTACACCGGGGGAGTCACTCGGAGGACTGCCGGTCTGGTACGTC
 W G H V A P S V S L L T P K P L Q
 Prostasin.CDS

601 CAACTCGAGGTGCCTCTGATCAGTCGTGAGACGTGTAAGTGCCTGTACAA
 -----+-----+-----+-----+-----+
 GTTGAGCTCCACGGAGACTAGTCAGCACTGACATTGACGGACATGTT
 Q L E V P L I S R E T C N C L Y N
 Prostasin.CDS

651 CATCGACGCCAAGCCTGAGGAGCCGCACTTGTCCAAGAGGAATGGTGT
 -----+-----+-----+-----+-----+
 GTAGCTGCCGGTTCGGACTCCTCGCGTGAACAGGTCTCCTGTACACCA
 I D A K P E E P H F V Q E D M V
 Prostasin.CDS

FIG. 3(C)

701 GTGCTGGCTATGTGGAGGGGGCAAGGACGCCCTGCCAGGGT~~GACTCTGGG~~
 -----+-----+-----+-----+-----+
 CACGACCGATACACCTCCCCCGTCCTGCCGACGGTCCC~~A~~CTGAGACCC
 C A G Y V E G G K D A C Q G D S G
 _____ Prostasin.CDS _____

751 GGCCCACCTCCTGCCCTGTGGAGGGTCTCTGGTACCTGAC~~GGGCATTGT~~
 -----+-----+-----+-----+-----+
 CGGGGTGAGAGGACGGGACACCTCCCAGAGACCATGGACT~~G~~CCCGTAACA
 G P L S C P V E G L W Y L T G I V
 _____ Prostasin.CDS _____

801 GAGCTGGGGAGATGCCTGTGGGGCCCGAACAGGCCTGGT~~G~~TGTACACTC
 -----+-----+-----+-----+-----+
 CTCGACCCCTCTACGGACACCCCGGGCGTTGTCCGGACCAC~~A~~CATGTGAG
 S W G D A C G A R N R P G V Y T
 _____ Prostasin.CDS _____

851 TGGCCTCCAGCTATGCCTCCTGGATCAAAGCAAGGTGAC~~A~~GAACCTCAG
 -----+-----+-----+-----+-----+
 ACCGGAGGTCGATAACGGAGGACCTAGGTTCTGTTCCACTG~~T~~CTTGAGGTC
 L A S S Y A S W I Q S K V T E L Q
 _____ Prostasin.CDS _____

901 CCTCGTGTGGTCCCCAAACCCAGGAGTCCCAGCCGAC~~A~~CAACCTCTG
 -----+-----+-----+-----+-----+
 GGAGCACACCAACGGGTTGGGTCTCAGGGTCGGGTG~~T~~CTTGGAGAC
 P R V V P Q T Q E S Q P D S N L C
 _____ Prostasin.CDS _____

951 Xba I
 TGGCAGCCACCTGGCCTTCAGCTAGACATCACCATCAC~~CC~~ATCACTAGC
 -----+-----+-----+-----+-----+
 ACCGTCGGTGGACCGGAAGTCGAGATCTGTAGTGGTAGTGG~~T~~AGTGTAGCG
 G S H L A F S | S R | H H H H H H *
 _____ Prostasin.CDS _____ 6 X HIS-TAG _____

1001 Not I
 GGCGGCTTCCCTTAGTGAGGGTAATGCTTCGAGCAGAC~~A~~TGATAAGAT
 -----+-----+-----+-----+-----+
 CGGGCGAAGGGAAATCACTCCCAATTACGAAGCTCGCTGTACTATTCTA

FIG. 3(D)

1051 ACATTGATGAGTTGGACAAACCACAACTAGAATGCAGTGA~~A~~~~A~~~~A~~~~A~~ATGC
 TGTAAC TACTCAAACCTGTTGGTGATCTTACGTCACT~~T~~TTTTTACG

SV40 Late pA

1101 TTTATTGTGAAATTGTGATGCTATTGCTTATTGTAAC~~C~~~~C~~~~C~~~~C~~ATTATAAG
 AAATAAACACTTAAACACTACGATAACGAAATAAACATT~~G~~~~G~~TAATATT~~C~~

1100

1150

SV40 Late pA

1151 CTGCAATAAACAAAGTTGAC
 GACGTTATTTGTTCAACTG

1169

FIG. 4(A)

SEQ.ID.NO.:8

Eco RI
 1 GAATTCAACCACCATGGCTTCCTCTGGCTCCCTCCTGCTGGGCCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGAGAGGACGACCCGGGAGGA
 M A F L W L L S C W A L L
 Chymotrypsinogen Pre

50

51 GGGTACCACTCGGCTGGGGTCCCCGACTACAAGGACGACGACGACG
 CCCATGGTGGAACCGACGCCCCAGGGCTGATGTTCTGCTGCTGCTGC
 G T T F G C G V P D Y K D D D D |
 Chymotrypsinogen Pre FLAG

100

101 Not I
 CGGCCGCTCTGCTGCCCTTGATGATGATGACAAGATCGTTGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTCTAGCAACCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

150

151 Xba I
 TATGCTCTAGAGGCCGGTCAGTGGCCCTGGCAGGTACAGCATCACCTATGA
 ATACGAGATCTCCGGCCAGTCACCGGGACCGTCCAGTCGTAGTGGATACT
 Y A L | E | A G Q W P W Q V S I T Y E
 Prostasin.CDS

200

201 AGGCCTCCATGTGTGGCTCTCGTGTCTGAGCAGTGGGTGCTGT
 TCCGCAGGTACACACACCACCGAGAGAGCACAGACTCGTCACCCACGACA
 G V H V C G G S L V S E Q W V L
 Prostasin.CDS

250

251 CAGCTGCTCACTGCTCCCCAGCGAGCACACAAGGAAGCCTATGAGGTC
 GTGACGAGTGAAGGGGTCGCTCGTGGTGTCCCTCGGATACTCCAG
 S A A H C F P S E H H K E A Y E V
 Prostasin.CDS

300

301 AAGCTGGGGCCCACCAAGCTAGACTCCTACTCCGAGGACGCCAAGGTCAG
 TTCGACCCCCGGTGGTCGATCTGAGGATGAGGCTCTCGGGTTCCAGTC
 K L G A H Q L D S Y S E D A K V S
 Prostasin.CDS

350

FIG. 4(B)

351 CACCCCTGAAGGACATCATCCCCCACCCAGCTACCTCCAGGAGGGCTCCC
 -----+-----+-----+-----+-----+
 GTGGGACTTCCTGTAGTAGGGGGTGGGTCGATGGAGGTCTCCCCGAGGG
 T L K D I I P H P S Y L Q E G S
 _____ Prostasin.CDS _____

400

401 AGGGCGACATTGCACTCCTCCAACTCAGCAGACCCATCACCTTCTCCGC
 -----+-----+-----+-----+
 TCCCCTGTAACGTGAGGAGGTTGAGTCGTCGGTAGTGGAAAGAGGGCG
 Q G D I A L L Q L S R P I T F S R
 _____ Prostasin.CDS _____

450

451 TACATCCGGCCATCTGCCCTGCAGCCAACGCCCTTCCCCAACGG
 -----+-----+-----+-----+
 ATGTAGGCCGGTAGACGGAGGGACGTCGGTGCGGAGGAAGGGGTGCC
 Y I R P I C L P A A N A S F P N G
 _____ Prostasin.CDS _____

500

501 CCTCCACTGCACTGTCACTGGCTGGGTCATGTGGCCCCCTCAGTGAGCC
 -----+-----+-----+-----+
 GGAGGTGACGTGACAGTGACCGACCCCAGTACACCGGGGAGTCACTCGG
 L H C T V T G W G H V A P S V S
 _____ Prostasin.CDS _____

550

551 TCCTGACGCCAAGCCACTGCAGCAACTCGAGGTGCCTCTGATCAGTCGT
 -----+-----+-----+-----+
 AGGACTGCAGGGTCGGTGACGTCGTTGAGCTCCACGGAGACTAGTCAGCA
 L L T P K P L Q Q L E V P L I S R
 _____ Prostasin.CDS _____

600

601 GAGACGTGTAACTGCCTGTACAACATCGACGCCAAGCCTGAGGAGCCGA
 -----+-----+-----+-----+
 CTCTGCACATTGACGGACATGTTGAGCTGCAGGGTCCGACTCCTCGGCGT
 E T C N C L Y N I D A K P E E P H
 _____ Prostasin.CDS _____

650

651 CTTTGTCCAAGAGGACATGGTGTGCTGGCTATGGAGGGGGCAAGG
 -----+-----+-----+-----+
 GAAACAGGTTCTCCTGTACCAACACGACCGATAACCTCCCCCGTCC
 F V Q E D M V C A G Y V E G G K
 _____ Prostasin.CDS _____

700

FIG. 4(C)

ACGCCTGCCAGGGTGA C T G G G G C C A C T C T C C T G C C C T **G T G G A G G G T**
 701 -----+-----+-----+-----+-----+
 TGC GG AC GGT CCC ACT GAG ACC C C C G G G T GAG AGG A C G G G A C A C C T C C A
 D A C Q G D S G G P L S C P V E G
 _____ Prostasin.CDS _____

CTCTGGTACCTGACGGGATTGTGAGCTGGGGAGATGCCT**G T G G G C C G**
 751 -----+-----+-----+-----+-----+
 GAG ACC ATGGACTGCCGTAACACTCGACCCCTCTACGGAC**A C C C G G G C**
 L W Y L T G I V S W G D A C G A R
 _____ Prostasin.CDS _____

CAACAGGCCTGGTGTGTACACTCTGGCCTCCAGCTATGCCT**C C T G G A T C C**
 801 -----+-----+-----+-----+-----+
 GTTGTCCGGACCACACATGTGAGACCGGAGGTCGATA CGGAG**G A C T A G G**
 N R P G V Y T L A S S Y A S W I
 _____ Prostasin.CDS _____

AAAGCAAGGTGACAGAACTCCAGCCTCGTGTGGTCCCCA**A A C C A G G A G**
 851 -----+-----+-----+-----+-----+
 TTTCGTTCCACTGTCTTGAGGTGGAGCACACCACGGGTT**T T G G G C C T C**
 Q S K V T E L Q P R V V P Q T Q E
 _____ Prostasin.CDS _____

Xba I
 TCCCAGCCCACAGCAACCTCTGTGGCAGCCACCTGGCCT**T C A G C T C A G**
 901 -----+-----+-----+-----+-----+
 AGGGTCGGGCTGTCGTTGGAGACACCGTCGGTGGACCGG**A G T C G A G A T C**
 S Q P D S N L C G S H L A F S | S R
 _____ Prostasin.CDS _____

Not I
 ACATCACCATCACCATCACTAGCGGCCGCTTCCCTTAGT**G A G G T A A T**
 951 -----+-----+-----+-----+-----+
 TGTAGTGGTAGTGGTAGT GATGCCGGCGAAGGGAAATCACT**T C C A A T T A**
 | H H H H H H * |
 6 X HIS-TAG _____

GCTTCGAGCAGACATGATAAGATACATTGATGAGTTGGAC**A A A C C A A A**
 1001 -----+-----+-----+-----+-----+
 CGAACGCTCGTCTGTACTATTCTATGTAAC T A C T C A A A C C T G T T T G G G T T

SV40 Late pA

FIG. 4(D)

1051 CTAGAATGCAGTGAAAAAAATGCTTATTGTGAAATTGT**GATGCTATT**
 -----+-----+-----+-----+-----+-----+
 GATCTTACGTCACTTTTACGAAATAAACACTTAAAC**A**CTACGATAA

SV40 Late pA

1101 GCTTATTTGTAACCATTATAAGCTGCAATAAACAGTT**GAC**
 -----+-----+-----+-----+-----+
 CGAAATAAACATTGGTAATATTCGACGTT**A**TTGTTCAACT**G**

1100 1142

FIG. 5(A)

SEQ.ID.NO.:9

Eco RI

1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAATCCCCTGCT
 CTTAAGTGGTGGTACCTGTCTTCCAAGCAGCGTCTTAGGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTCAAATCTACTCTTGTGCCAGGGTGTGGCTCCG
 GGACGACGACCACACAGTTAGATGAGAACACGGTCCCACACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

100

101 Not I

ACTACAAGGACGACGACGTGGACGCCGCTTGCTGCCCTTT
 TGATGTTCTGCTGCTGCACCTGCACGGCGAGAACGACGGGGAAA
 D Y K D D D D V D A A A L A A P F
 FLAG EK1 Pro

150

151 Xba I

GATGATGATGACAAGATCGTGGGGCTACAACGTCTAGAAACCCATT
 CTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCTGGGTAAG
 D D D D K I V G G Y N C L E P H S
 EK1 Pro

200

201

GCAGCCTTGGCAGGCCCTTGTCCAGGCCAGCAACTACTCTGGCG
 CGTCGGAACCGTCCGCCGAACAAGTCCGGTCGTGATGAAGACACCGC
 Q P W Q A A L F Q G Q Q L L C G
 Neuropsin.CDS

250

251

GTGTCTTGTAGGTGGCAACTGGGTCTTACAGCTGCCACTGTAAAAAA
 CACAGGAACATCCACCGTTGACCCAGGAATGTCGACGGGTGACATTTTT
 G V L V G G N W V L T A A H C K K
 Neuropsin.CDS

300

301

CCGAAATAACACAGTACGCCCTGGGAGACCACAGCCTACAGAAATAAAGATGG
 GGCTTTATGTGTCACTGCCACCCCTCTGGTGTGGATGTCTTATTTCTACC
 P K Y T V R L G D H S L Q N K D G
 Neuropsin.CDS

350

FIG. 5(B)

+-----+-----+-----+-----+-----+

351 CCCAGAGCAAGAAATACCTGTGGTTAGTCATCCCACACC CCTGCTACA
 -----+-----+-----+-----+-----+
 GGGTCTCGTTCTTATGGACACCAAGTCAGGTAGGGTGTGG GGACCATGT
 P E Q E I P V V Q S I P H P C Y
Neuropsin.CDS

400

401 ACAGCAGCGATGTGGAGGACCAACCATGATCTGATGCTT C TTCACTG
 -----+-----+-----+-----+-----+
 TGTCGTCGCTACACCTCCTGGTGTGGTACTAGACTACGAAGAAGTTGAC
 N S S D V E D H N H D L M L L Q L
Neuropsin.CDS

450

451 CGTGACCAGGCATCCCTGGGTCAAAGTGAAGCCCATCAG CCTGGCAGA
 -----+-----+-----+-----+-----+
 GCACTGGTCCGTAGGGACCCAGGTTCACTTCGGTAGTC GGACCGTCT
 R D Q A S L G S K V K P I S L A D
Neuropsin.CDS

500

501 TCATTGCACCCAGCCTGGCCAGAAGTGCACCGTCTCAGGCT GGGGACTG
 -----+-----+-----+-----+-----+
 AGTAACGTGGGTGGACCCGGTCTCACGTGGCAGAGTCGA ACCCGTGAC
 H C T Q P G Q K C T V S G W G T
Neuropsin.CDS

550

551 TCACCAGCCCCAGAGAGAATTTCTGACACTCTCACTGT GCAGAAGTA
 -----+-----+-----+-----+-----+
 AGTGGTCAGGGGCTCTCTAAAAGGACTGTGAGAGTTGACAC GTCTTCAT
 V T S P R E N F P D T L N C A E V
Neuropsin.CDS

600

601 AAAATCTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGG GCAGATCAC
 -----+-----+-----+-----+-----+
 TTTTAGAAAGGGTCTCTCACACTCCTACGAATGGGCC CGTCTAGTG
 K I F P Q K K C E D A Y P G Q I T
Neuropsin.CDS

650

651 AGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGCTGACAC GTGCCAGG
 -----+-----+-----+-----+-----+
 TCTACCGTACCAAGACACGTCCGTCTCGTTCCCGACTGT GCACGGTCC
 D G M V C A G S S K G A D T C Q
Neuropsin.CDS

700

FIG. 5(C)

701 GCGATTCTGGAGGCCCTGGTGTGATGGTGCACCCAGGGCATCACA
 CGCTAACGACTCCGGGGGACCACACACTACCACGTGAGGTCCCGTAGTGT
 G D S G G P L V C D G A L Q G I T
Neuropsin.CDS

751 TCCTGGGCTCAGACCCCTGTGGAGGTCCGACAAACTGGCGTCTATAC
 AGGACCCCGAGTCTGGGACACCCCTCCAGGCTGTTGGACCAGATATG
 S W G S D P C G R S D K P G V Y T
Neuropsin.CDS

801 CAACATCTGCCGCTACCTGGACTGGATCAAGAAGATCATAGGCAAGG
 GTTGTAGACGGCGATGGACCTGACCTAGTTCTTAGTATCCCGTGTCC
 N I C R Y L D W I K K I I G S K
Neuropsin.CDS

851 Xba I Not I
 GCTCTAGACATCACCATCACCATCACTAGCGGCCCTCCC TTAGTGAG
 CGAGATCTGTAGTGGTAGTGGTAGTGTATCGCCGGGAAGGGAAATCACTC
 G | S R | H H H H H H * |
 6 X HIS-TAG

901 GGTAAATGCTTCGAGCAGACATGATAAGATACATTGATGAGTTGGACAA
 CCAATTACGAAGCTCGTCTGTACTATTCTATGTAACACTCAAACTGT
SV40 Late pA

951 ACCACAACTAGAATGCAGTGAAAAAAATGCTTATTGTGAAATTGTGA
 TGGTGTGATCTACGTCACTTTTACGAAATAAACACTTTAAACACT
SV40 Late pA

1001 TGCTATTGCTTATTGTAAACCATTATAAGCTGCAATAAACAAAGTGAC
 ACGATAACGAAATAAACATTGGTAATATTGACGTTATTGTTCACGT
SV40 Late pA

22/34

FIG. 6(A)

SEQ.ID.NO.:10

Eco RI
GAATT CACCACCATGGACAGCAAAGGTTCGTCGCAGAAATC CCGCTGCT
1 -----+-----+-----+-----+-----+-----+
CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTAG GGCGGACGA
M D S K G S S Q K S R L L
Prolactin Signal Sequence

50

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGTG TGGCTCCG
-----+-----+-----+-----+-----+-----+
GGACGACGACCACCAACAGTTAGATGAGAACACGGTCCCAC ACCAGAGGC
L L L V V S N L L L C Q G V V S
Prolactin Signal Sequence

100

101 Not I
ACTACAAGGACGACGACGTGGACGCGCCGCTTGCT GCCCCTTT
-----+-----+-----+-----+-----+
TGATGTTCCCTGCTGCTGCTGCACCTGCGCCGGCGAGAACGACGGGGAAA
D Y K D D D D V D A A A A L A A P F
FLAG EK1 Pro

150

151 Xba I
GATGATGACAAGATCGTTGGGGCTACAACCTGCTAGA AAAGCACTC
-----+-----+-----+-----+-----+
CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCT TTTCGTGAG
D D D D K I V G G Y N C L E K H S
EK1 Pro

200

201 CCAGCCCTGGCAGGCAGCCCTGTTCGAGAACGCGGCTACTCTGGGG
-----+-----+-----+-----+-----+
GGTCGGGACCGTCCGTCGGGACAAGCTCTGCGCCGATGAGACACCCC
Q P W Q A A L F E K T R L L C G
Protease O.CDS

250

251 CGACGCTCATCGCCCCCAGATGGCTCCTGACAGCAGCCACTGCTCAAG
-----+-----+-----+-----+-----+
GCTGCGAGTAGCGGGGGCTACCGAGGACTGTCGTCGGGTGACGGAGTTC
A T L I A P R W L L T A A H C L K
Protease O.CDS

300

301 CCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAAAGGAGGAGGG
-----+-----+-----+-----+-----+
GGGGCGATGTATCAAGTGGACCCCGTCGTGTTGGAGGTCTT CCTCCCTCCC
P R Y I V H L G Q H N L Q K E E G
Protease O.CDS

350

FIG. 6(B)

CTGTGAGCAGACCCGGACAGCCACTGAGTCCTTCCCCACCC CGGCTCA
 351 -----+-----+-----+-----+-----+
 GACACTCGTCTGGGCCTGTCGGTGACTCAGGAAGGGGGGGGCCGA
 C E Q T R T A T E S F P H P G F
 _____ Protease O.CDS _____

400

ACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATGC TGGTAAG
 401 -----+-----+-----+-----+-----+
 TGTTGTCGGAGGGGTTGTTCTGGTGGCGTTACTGTAGTACG ACCACTC
 N N S L P N K D H R N D I M L V K
 _____ Protease O.CDS _____

450

ATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTC ACCCTTC
 451 -----+-----+-----+-----+-----+
 TACCGTAGCGGTCAAGAGGTAGTGGACCCGACACGCTGGGAG TGGGAGAG
 M A S P V S I T W A V R P L T L S
 _____ Protease O.CDS _____

500

CTCACGCTGTCACTGCTGGCACCAAGCTGCCTCATTCCGGCTGGGCA
 501 -----+-----+-----+-----+-----+
 GAGTGCACACAGTGACGACCGTGGTCACGGAGTAAAGGCC ACCCGT
 S R C V T A G T S C L I S G W G
 _____ Protease O.CDS _____

550

GCACGTCCAGCCCCAGTTACGCCCTCACACCTTGCAT GCGAAC
 551 -----+-----+-----+-----+
 CGTGCAGGTGGGGTCAATGCGGACGGAGTGTGGAACGCTACGCCGTTG
 S T S S P Q L R L P H T L R C A N
 _____ Protease O.CDS _____

600

ATCACCATCATTGAGCACAGAAGTGTGAGAACGCCACCCGGCAACAT
 601 -----+-----+-----+-----+
 TAGTGGTAGTAACCTCGTGGTCTTCACACTCTTGCAGGGCCGGTGA
 I T I I E H Q K C E N A Y P G N I
 _____ Protease O.CDS _____

650

CACAGACACCAGGTGTGCCAGCGTGCAGGAAGGGGGCAAGGACTCT
 651 -----+-----+-----+-----+
 GTGTCGTGGTACACACACGGTGGCACGTCTTCCCCGTTCCCTGAGGA
 T D T M V C A S V Q E G G K D S
 _____ Protease O.CDS _____

700

FIG. 6(C)

4 O'clock
10 o'clock
2 o'clock
8 o'clock
12 o'clock
6 o'clock

701 GCCAGGGTGAECTCCGGGGCCCTCTGGTCTGTAACCAGTCT C TTCAAGGC -----+-----+-----+-----+-----+ CGGTCCCACGTAGGGCCCCGGGAGACAGACATTGGTCAGA G AAGTTCCG C Q G D S G G P L V C N Q S L Q G <u>Protease O.CDS</u>	750
751 ATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCGAA A GCCTGGTGT -----+-----+-----+-----+-----+ TAATAGAGGACCCCGGTCTAGGCACACGCTAGTGGGTTT T CGGACCACA I I S W G Q D P C A I T R K P G V <u>Protease O.CDS</u>	800
801 CTACACGAAAGTCTGCAAATATGTGGACTGGATCCAGGAG A CGATGAAGA -----+-----+-----+-----+-----+ GATGTGCTTTCAGACGTTATACACCTGACCTAGGTCTCT T GCTACTTCT Y T K V C K Y V D W I Q E T M K <u>Protease O.CDS</u>	850
851 <u>Xba I</u> <u>Not I</u> ACAATTCTAGACATCACCATCACCATCACTAGCGCCGCT T CCCTTAGT -----+-----+-----+-----+-----+ TGTAAAGATCTGTAGTGGTAGTGGTAGTGA T CGCCGGCGA A GGGAATCA N N S R H H H H H H * <u>6 X HIS-TAG</u>	900
901 GAGGGTTAACGCTTCGAGCAGACATGATAAGATACTTGAT T GAGTTGGA -----+-----+-----+-----+-----+ CTCCCAATTACGAAGCTCGTCTGTACTATTCTATGTA T ACTCAAACCT <u>SV40 Late pA</u>	950
951 CAAACACAACTAGAACATGCAGTGAAAAAAATGCTTATTG T TGAAATTG -----+-----+-----+-----+-----+ GTTTGGTGTGATCTACGTCACTTTTTACGAAATAACACTTTAAC <u>SV40 Late pA</u>	1000
1001 TGATGCTATTGCTTATTGTAACCATTATAAGCTGCAAT A AAACAAGTTG -----+-----+-----+-----+-----+ ACTACGATAACGAAATAAACATTGGTAATATTGACGTTATTTGTTAAC <u>SV40 Late pA</u>	1050
1051 AC -- 1052 TG	

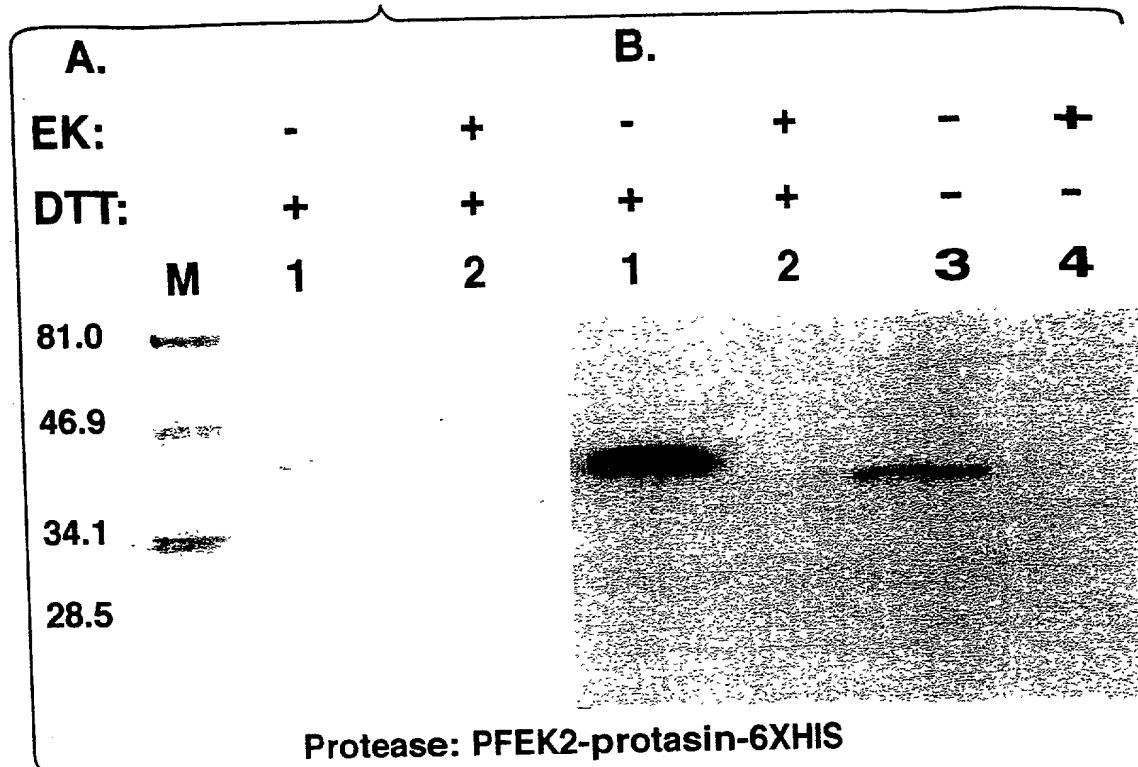
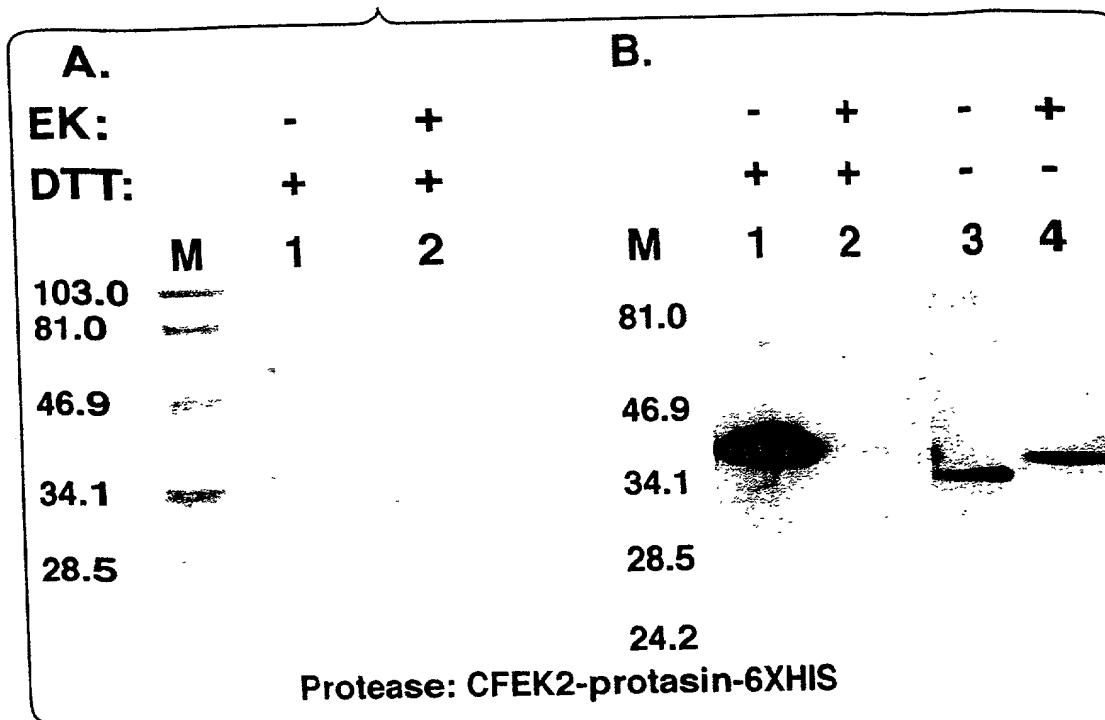
FIG. 7**FIG. 8**

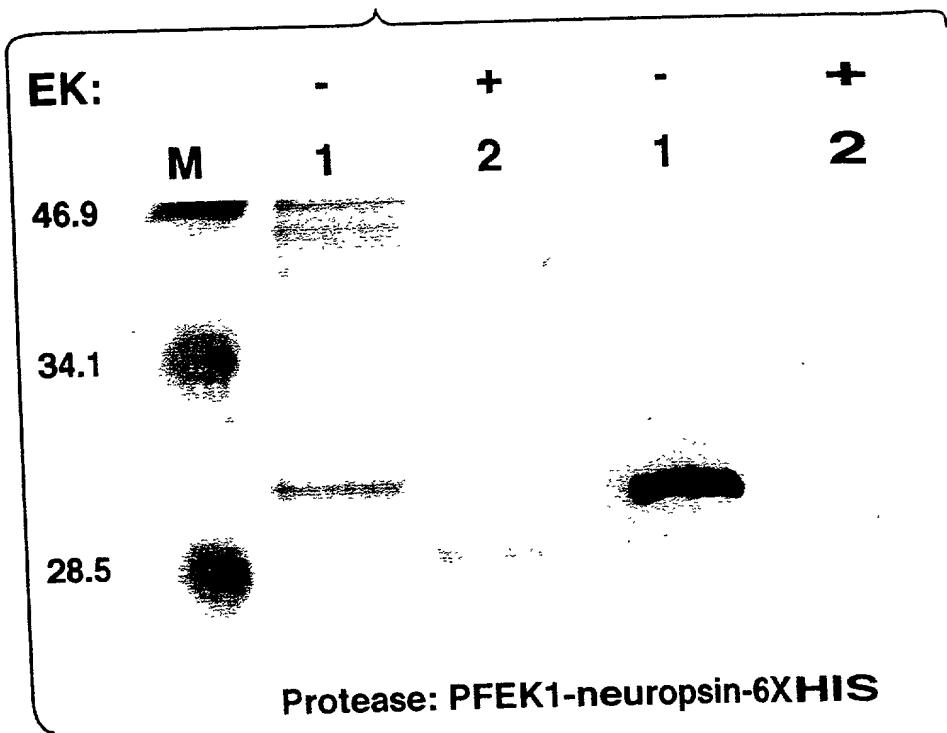
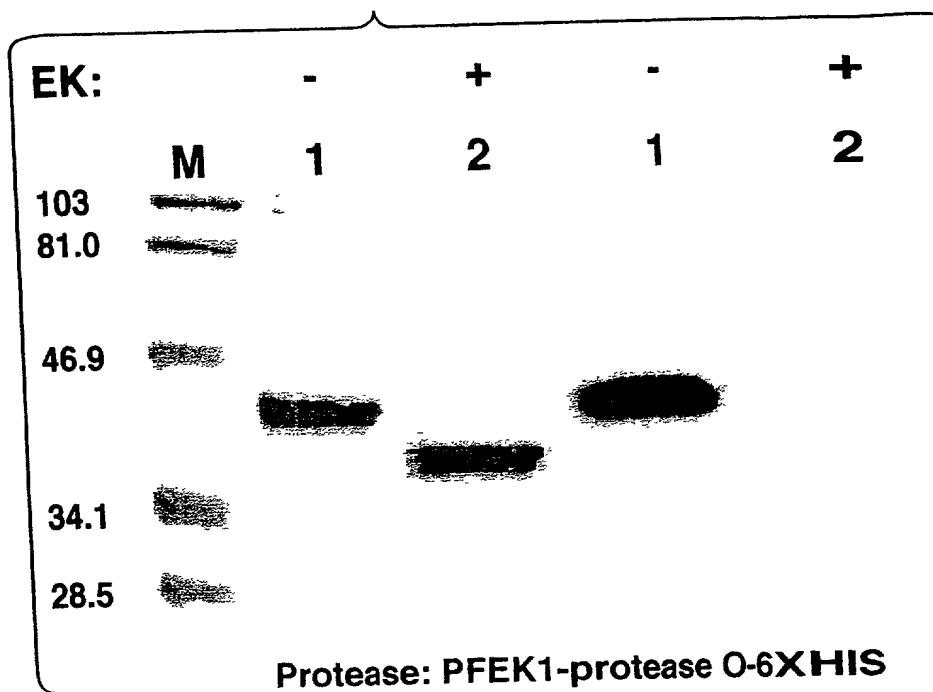
FIG. 9**FIG. 10**

FIG. 11

EK:

- + -

M 1 2 1

46.9

34.1

28.5

Protease: CFEK2-Protease F-6XHIS

FIG. 12

EK:

- + -

M 1 2 1

103

81.0

46.9

34.1

28.5

Protease: PFEK-MH2-6XHIS

FIG. 13(A)

SEQ.ID.NO.:53

Eco RI
 1 GAATTCAACCACCATGGCTTCCTCTGGCTCCTCTCCGCTG**G G**GCCTCCT
 CTTAAGTGGTGGTACCGAAAGGAGACCGAGGAGAGGACG**A C**CGGGAGGA
 M A F L W L L S C W A I L
 Chymotrypsinogen Pre

50

GGGTACCACCTCGGCTGGGGTCCCCGACTACAAGGACG**A C**CGACGACG
 51 CCCATGGTGGAAAGCCGACGCCAGGGCTGATGTTCTGC**T G**CTGCTGC
 G T T F G C G V P D Y K D D D D
 Chymotrypsinogen Pre FLAG

100

Not I
 101 CGGCCGCTCTTGCTGCCCTTGATGATGATGACAAGATC**G T**TGGGGC
 GCCGGCGAGAACGACGGGGAAACTACTACTACTGTTCTAG**C A**ACCCCCG
 A A A L A A P F D D D D K I V G G
 EK2 Pro

150

Xba I
 151 TATGCTCTAGAACTCGGGCGTTGGCCGTGGCAGGGAGC**T G**CGCTGTG
 ATACGAGATCTTGAGCCGCAACCGCACCGTCCCTCGG**A C**CGGGACAC
 Y A L E L G R W P W Q G S L R I W
 Protease F.CDS

200

201 GGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCG**T G**GGCACTCA
 CCTAAGGGTGCATACGCCCACTCGGACGAGTCGGTGGCG**A C**CCGTGAGT
 D S H V C G V S L L S H R W A L
 Protease F.CDS

250

251 CGGCGGCGACTGCTTGAAACCTATAGTGACCTTAGTGAT**C C**CTGGGG
 GCCGCCGCGTGACGAAACTTGATATCACTGGAATCACT**A G**GGGAGGCC
 T A A H C F E T Y S D L S D P S G
 Protease F.CDS

300

301 TGGATGGTCCAGTTGGCCAGCTGACTCCATGCCATC**T C**TGGAGCCT
 ACCTACCAGGTCAAACCGGTGACTGAAGGTACGGTAGGA**A G**ACCTGGGA
 W M V Q F G Q L T S M P S F W S L
 Protease F.CDS

350

FIG. 13(B)

351 GCAGGCCTACTACAACCGTTACTCGTATCGAATATCTATCT**GAGCCCTC**
 CGTCGGGATGATGTTGGCAATGAAGCATAGCTTATAGATAGACT**TGGGAG**
 Q A Y Y N R Y F V S N I Y L S P
 _____ Protease F.CDS _____

401 GCTACCTGGGAATTCACCTATGACATTGCCCTGGTGAAGCT**GTCTGCA**
 CGATGGACCCCTTAAGTGGATACTGTAACGGAACC**ACTTCGACAGAC**
 R Y L G N S P Y D I A L V K L S A
 _____ Protease F.CDS _____

451 CCTGTCACCTACACTAAACACATCCAGCCC**ATCTGTCTCCAGGCCCTCAC**
 GGACAGTGGATGTGATTGTGAGGT**CGGGTAGACAGAGGTCCGGAGGTG**
 P V T Y T K H I Q P I C L Q A S T
 _____ Protease F.CDS _____

501 ATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGG**CTGGGGTACA**
 TAAACTCAA**ACTCTGGCCTGTCTGACGACCCACTGACCGACC**CCC**CATGT**
 F E F E N R T D C W V T G W G Y
 _____ Protease F.CDS _____

551 TCAAAGAGGATGAGGC**ACTGCCATCTCCCCACACCC**CTCCAG**GAAGTTCAG**
 AGTTTCTC**CTACTCCGTGACGGTAGAGGGGTGTGGAGGT**CC**TTCAGTC**
 I K E D E A L P S P H T L Q E V Q
 _____ Protease F.CDS _____

601 GTCGCCATCAT**AAACAAC**TCTATGTGCAACC**ACCTCTCCTCAAGTACAG**
 CAGCGGTAGTATTGTTGAGATA**ACGTTGGTGGAGAAGGAGT**T**CATGTC**
 V A I I N N S M C N H L F L K Y S
 _____ Protease F.CDS _____

651 TTTCCGCAAGGACATCTTGGAGACATGGTTGTGCTGG**CAATGCCAAG**
 AAAGGC**GTTCTGTAGAAACCTCTGTACCAAACACGACCGTTACGGGT**TC
 F R K D I F G D M V C A G N A Q
 _____ Protease F.CDS _____

FIG. 13(C)

701 GCGGGAAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTG **G C C T G T A A C**
 CGCCCTTACGGACGAAGCCACTGAGTCCACCTGGGAAC **C G G A C A T T G**
 G G K D A C F G D S G G P L A C N
 Protease F.CDS

751 AAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGG **A G T G G G C T G**
 TTCTTACCTGACACCATACTAACCTCAGCACTCGACCCCC **T C A C C C G A C**
 K N G L W Y Q I G V V S W G V G C
 Protease F.CDS

801 TGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCC **A C C A C T T G**
 ACCAGCCGGGTTAGCCGGGCCACAGATGTGGTTATAGTCGG **T G G T G A A C**
 G R P N R P G V Y T N I S H H F
 Protease F.CDS

851 AGTGGATCCAGAAGCTGATGGCCCAGAGTGGCATGTCCCAG **C C A G A C C C**
 TCACCTAGGTCTCGACTACCGGGTCTCACCGTACAGGGTC **G G T C T G G G G**
 E W I Q K L M A Q S G M S Q P D P
 Protease F.CDS

901 Xba I Not I
 TCCTGGTCTAGACATCACCATCACCATCACTAGCGGGCCT **T T C C C T T A G**
 AGGACCAGATCTGTAGTGGTAGTGGTAGTGA **T C G C C G G C G A A G G G A A T C**
 S W | S R | H H H H H H *] _____
 6 X HIS-TAG

951 TGAGGGTTAATGCTTCGAGCAGACATGATAAGATACTTGAT **G A G T T G G**
 ACTCCCAATTACGAAGCTCGTCTGTACTATTCTATGTA **A C T A C T C A A A C C**
 SV40 Late pA

1001 ACAAAACACAACTAGAATGCAGTAAAAAAATGCTTATTTGTGAATT
 TGTTGGTGTGATCTTACGTCACTTTTTACGAAATAACACTTTAAA
 SV40 Late pA

1051 GTGATGCTATTGCTTATTTGTAACCATTATAAGCTGCAAT **A A A C A A G T T**
 CACTACGATAACGAAATAAACATTGGTAATATTGACGTT **A T T T G T C A A**
 SV40 Late pA

FIG. 13(D)

1101 GAC

 CTG 1103

SEQ. ID.NO.:54

FIG. 14(A)

Eco RI
 1 GAATTCAACCACCATGGACAGCAAAGGTTCGTCGCAGAAAT C CCGCTGCT
 CTTAAGTGGTGGTACCTGTCGTTCCAAGCAGCGTCTTA GGGCGGACGA
 M D S K G S S Q K S R L L
 Prolactin Signal Sequence

51 CCTGCTGCTGGTGGTGTCAAATCTACTCTTGTGCCAGGGT G T G G T C C G
 GGACGACGACCACACAGTTAGATGAGAACACGGTCCCAC ACCAGAGGC
 L L L V V S N L L L C Q G V V S
 Prolactin Signal Sequence

101 Not I
 ACTACAAGGACGACGACGTGGACGCGCCGCTTGCT G C C C C P T T
 TGATGTTCCCTGCTGCTGCTGCACCTGCGCCGGCGAGAACG A C G G G G A A A
 D Y K D D D D V D A A A L A A P F
 FLAG EK1 Pro

151 Xba I
 GATGATGATGACAAGATCGTTGGGGCTACAACTGTCTAG A G C C G C A C T C
 CTACTACTACTGTTCTAGCAACCCCCGATGTTGACAGATCT C G G C T G A G
 D D D D K I V G G Y N C L E P H S
 EK1 Pro

201 GCAGCCCTGGCAGGCGGACTGGTCATGGAAAACGAATTG T T C T G C G G
 CGTCGGGACCGTCCGCCGTGACCACTTGTCTAACAAAGACGAGCC
 Q P W Q A A L V M E N E L F C S
 MH2.CDS

251 GCGTCCTGGTGCATCCGCAGTGGGTGCTGTCAGCCGACAC T G T T C C A G
 CGCAGGACACGTAGGCGTCACCCACGACAGTCGGGTGT G A C A A G G T C
 G V L V H P Q W V L S A A H C F Q
 MH2.CDS

301 AACTCCTACACCACGGGCTGGGCTGCACAGTCTTGAGG C C G A C C A A G A
 TTGAGGGATGTGGTAGCCGACCCGGACGTGTCAGAACTCC G G C T G G T C T
 N S Y T I G L G L H S L E A D Q E
 MH2.CDS

FIG. 14(B)

351 GCCAGGGAGCCAGATGGTGGAGGCCAGCCTCTCCGTACGGCACCCAGT
 400 CGGTCCCTCGGTCTACCACCTCCGGTCGGAGAGGCATGCCGTGGGTCA
 P G S Q M V E A S L S V R H P E
 _____ MH2.CDS _____

401 ACAACAGACCCTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAA
 450 TGTTGTCTGGGAACGAGCGATTGCTGGAGTACGAGTAGTTCAAACCTGCTT
 Y N R P L L A N D L M L I K L D E
 _____ MH2.CDS _____

451 TCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTGCAGTG
 500 AGGCACAGGCTCAGACTGTGGTAGGCCCTCGTAGTCGTAACGAAAGCGCAC
 S V S E S D T I R S I S I A S Q C
 _____ MH2.CDS _____

501 CCCTACCGCGGGGAACCTTGCCCTCGTTCTGGCTGGGTCTGCTGGGA
 550 GGGATGGCGCCCTTGAGAACGGAGCAAAGACCGACCCAGACGACCGCT
 P T A G N S C L V S G W G L L A
 _____ MH2.CDS _____

551 ACGGCAGAATGCCTACCGTGCTGCAGTGCCTGAAACGTGCGGTGGTGGTCT
 600 TGCGTCTTACGGATGGCACGACGTACGCACAGCCACCAAGAGA
 N G R M P T V L Q C V N V S V V S
 _____ MH2.CDS _____

601 GAGGAGGTCTGCAGTAAGCTCTATGACCCGCTGTACCAACCCAGCATGTT
 650 CTCCTCCAGACGTCAATTGAGATACTGGGCACATGGTGGGGTGTGACAA
 E E V C S K L Y D P L Y H P S M F
 _____ MH2.CDS _____

651 CTGCCGCCGGAGGGCACGACCAGAAGGACTCCTGCAACGGTGA
 700 GACGCCGCCCTCCGTGGTCTTCCCTGAGGACGGTGCACACTGAGAC
 C A G G H D Q K D S C N G D S
 _____ MH2.CDS _____

FIG. 14(C)

701 GGGGGCCCCTGATCTGCAACGGGTACTTGCAGGGCCTGTG **T** CTTGG
 750 CCCCCGGGGACTAGACGTTGCCATGAACGTCCCGAACAC **A** GAAGCT
 G G P L I C N G Y L Q G L V S F G
 MH2.CDS

751 AAAGCCCCGTGTGGCCAAGTTGGCGTGCAGGTGTACAC **C** AACCTCTG
 800 TTTGGGGCACACCGGTTCAACCGCACGGTCCACAGATGTG **G** GTGGAGAC
 K A P C G Q V G V P G V Y T N L C
 MH2.CDS

801 CAAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTT **C** TAGACATC
 850 GTTAAGTGAACCTATCTCTTGGCAGGTCCGGTCAA **A** GATCTGTAG
 K F T E W I E K T V Q A S | S R H
 MH2.CDS

851 ACCATCACCATCACTAGCGCCGCTTCCCTTACTGAGGGT **T** AATGTT
 900 TGGTAGTGGTAGTGATCGCCGGCGAAGGGAAATCACTCC **A** ATACGAAG
 H H H H H *
 — 6 X HIS-TAG —

901 GAGCAGACATGATAAGATAACATTGATGAGTTGGACAACC **A** CACTAGA
 950 CTCGTCTGTACTATTCTATGTAACACTCAAACCTGTTGG **T** GTGATCT
 SV40 Late pA

951 ATGCAGTAAAAAAATGCTTATTTGTGAAATTGTGATGC **T** ATTGTT
 1000 TACGTCACTTTTACGAAATAAACACTTAAACACTACG **A** TAACGAAA

1001 ATTTGTAACCATTATAAGCTGCAATAAACAAAGTTGAC
 1037 TAAACATTGTTAATATTGACGTTATTGTTCAACTG